



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/910,009

Source:

8/1/2001

Date Processed by STIC:

O/PK

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OICE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/910,009

DATE: 08/01/2001
TIME: 15:38:10

Input Set : A:\2314-242.ST25.txt
Output Set: N:\CRF3\08012001\I910009.raw

*see
pp. 5, 2-4*

Does Not Comply
Corrected Diskette Needed

OK

3 <110> APPLICANT: University of Utah Research Foundation
4 Cognetix, Inc.
5 Olivera, Baldomero M.
6 McIntosh, J. Michael
7 Garrett, James E.
8 Watkins, Maren
9 Cruz, Lourdes J.
10 Shon, Ki-Joon
11 Jacobsen, Richard
12 Jones, Robert M.
13 Cartier, G. Edward
14 Shen, Greg S.
15 Wagstaff, John D.
17 <120> TITLE OF INVENTION: Mu-Conopeptides
19 <130> FILE REFERENCE: 2314-242
21 <140> CURRENT APPLICATION NUMBER: US/09/910,009
21 <141> CURRENT FILING DATE: 2001-07-23
21 <150> PRIOR APPLICATION NUMBER: US 60/219,619
22 <151> PRIOR FILING DATE: 2000-07-21
24 <150> PRIOR APPLICATION NUMBER: US 60/245,157
25 <151> PRIOR FILING DATE: 2000-11-03
27 <150> PRIOR APPLICATION NUMBER: US 60/264,319
28 <151> PRIOR FILING DATE: 2001-01-29
30 <150> PRIOR APPLICATION NUMBER: US 60/277,270
31 <151> PRIOR FILING DATE: 2001-03-21
33 <160> NUMBER OF SEQ ID NOS: 520
35 <170> SOFTWARE: PatentIn version 3.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 280
39 <212> TYPE: DNA
40 <213> ORGANISM: Conus arentus
42 <400> SEQUENCE: 1
43 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttcttga ccatctgtat 60
45 gcttctgttt ccccttactg ctcttccgct ggatggggat caacctgcag accgacctgc 120
47 agagcgtatg caggacgaact ttataactga gcatcatccc ctgtttgatc ctgtcaaacy 180
49 gtgttgcgag aggccatgca acataggatg cgtaccttgt tgtaaatgac cagctttgtc 240
51 atcgcggcct catcaagcga ataagtaaaa cgattgcagt 280
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 67
56 <212> TYPE: PRT
57 <213> ORGANISM: Conus arentus
59 <400> SEQUENCE: 2
61 Met Met Ser Lys Leu Gly Val Phe Leu Thr Ile Cys Met Leu Leu Phe
62 1 5 10 15
64 Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
65 20 25 30
67 Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

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68 35 40 45
70 Asp Pro Val Lys Arg Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val
71 50 55 60
73 Pro Cys Cys
74 65
76 <210> SEQ ID NO: 3
77 <211> LENGTH: 14
78 <212> TYPE: PRT
79 <213> ORGANISM: Conus arentus
81 <220> FEATURE:
82 <221> NAME/KEY: PEPTIDE
83 <222> LOCATION: (1)..(14)
84 <223> OTHER INFORMATION: Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue
5 an
85 d 12 is Pro or (Hy)? what is this?
88 <400> SEQUENCE: 3
W--> 90 Cys Cys Xaa Arg Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
91 1 5 10
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 244
95 <212> TYPE: DNA
96 <213> ORGANISM: Conus atlanticus
98 <400> SEQUENCE: 4
99 ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctgcttct gtttccactt 60
101 actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120
103 atttcatctg atcaacatct cttctttgat ctcataaac ggtgctgcga gttgccatgc 180
105 gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240
107 cgag 244
110 <210> SEQ ID NO: 5
111 <211> LENGTH: 69
112 <212> TYPE: PRT
113 <213> ORGANISM: Conus atlanticus
115 <400> SEQUENCE: 5
117 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
118 1 5 10 15
120 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
121 20 25 30
123 Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
124 35 40 45
126 Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
127 50 55 60
129 Cys Val Pro Cys Cys
130 65
132 <210> SEQ ID NO: 6
133 <211> LENGTH: 15
134 <212> TYPE: PRT
135 <213> ORGANISM: Conus atlanticus
137 <220> FEATURE:
138 <221> NAME/KEY: PEPTIDE
139 <222> LOCATION: (1)..(15)

RAW SEQUENCE LISTING

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140 <223> OTHER INFORMATION: Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8

141 and 13 is Pro or Hy?

144 <400> SEQUENCE: 6

W--> 146 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys

147 1 - 5 10 15

149 <210> SEQ ID NO: 7

150 <211> LENGTH: 310

151 <212> TYPE: DNA

152 <213> ORGANISM: Conus aurisiacus

154 <400> SEQUENCE: 7

155 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgttt 60

157 gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctga 120

159 agagcgtatg caggacgaca ttcatctga gcagcatccc ttgtttaatc agaaaagaat 180

161 gtgttgccgc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg 240

163 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300

165 cgattgcagt 310

168 <210> SEQ ID NO: 8

169 <211> LENGTH: 74

170 <212> TYPE: PRT

171 <213> ORGANISM: Conus aurisiacus

173 <400> SEQUENCE: 8

175 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe

176 1 5 10 15

178 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro

179 20 25 30

181 Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe

182 35 40 45

184 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr

185 50 55 60

187 Phe Arg Asn Ser Gln Ile Cys His Cys Cys

188 65 70

190 <210> SEQ ID NO: 9

191 <211> LENGTH: 22

192 <212> TYPE: PRT

193 <213> ORGANISM: Conus aurisiacus

195 <220> FEATURE:

196 <221> NAME/KEY: PEPTIDE

197 <222> LOCATION: (1)..(22)

198 <223> OTHER INFORMATION: Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i

199 s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,

200 di-iodo-Tyr, O-sulpho-Tyr or O-phospho Ty Tyr

203 <400> SEQUENCE: 9

W--> 205 Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser

206 1 5 10 15

208 Gln Ile Cys His Cys Cys

209 20

211 <210> SEQ ID NO: 10

212 <211> LENGTH: 257

213 <212> TYPE: DNA

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Input Set : A:\2314-242.ST25.txt

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214 <213> ORGANISM: Conus aurisiacus

216 <400> SEQUENCE: 10

217	ggatccatga	tgtctaaact	gggagtccttg	ttgaccatct	gtttgcttct	gtttccctt	60
219	actgctcttc	cgatcgatgg	agatcaatct	gtagaccgac	ctgcagagcg	tatgcaggat	120
221	gacatttcat	ctgagcagca	tcgcttggtc	aatcagaaaa	gaagggtgctg	ccggtggcca	180
223	tgcccccgac	aaatcgacgg	tgaatattgt	ggctgttgcc	ttggatgata	accgtgttga	240
225	tgaccaactt	tctcgag					257

228 <210> SEQ ID NO: 11

229 <211> LENGTH: 75

230 <212> TYPE: PRT

231 <213> ORGANISM: Conus aurisiacus

233 <400> SEQUENCE: 11

235	Gly	Ser	Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu
236	1				5					10					15	
238	Leu	Phe	Pro	Leu	Thr	Ala	Leu	Pro	Ile	Asp	Gly	Asp	Gln	Ser	Val	Asp
239			20					25				30				
241	Arg	Pro	Ala	Glu	Arg	Met	Gln	Asp	Asp	Ile	Ser	Ser	Glu	Gln	His	Arg
242			35				40					45				
244	Leu	Phe	Asn	Gln	Lys	Arg	Arg	Cys	Cys	Arg	Trp	Pro	Cys	Pro	Arg	Gln
245		50				55					60					
247	Ile	Asp	Gly	Glu	Tyr	Cys	Gly	Cys	Cys	Leu	Gly					
248	65				70					75						

250 <210> SEQ ID NO: 12

251 <211> LENGTH: 19

252 <212> TYPE: PRT

253 <213> ORGANISM: Conus aurisiacus

255 <220> FEATURE:

256 <221> NAME/KEY: PEPTIDE

257 <222> LOCATION: (1)..(19)

258 <223> OTHER INFORMATION: Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3a → Arg is at location 3

259 nd 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho
 260 -Tyr or O-phospho-Tyr
 261 Tyr?

264 <400> SEQUENCE: 12

W--> 266 Cys Cys Arg Xaa Xaa Cys Xaa Arg Gln Ile Asp Gly Xaa Xaa Cys Gly

267	1			5			10					15
-----	---	--	--	---	--	--	----	--	--	--	--	----

269 Cys Cys Leu

272 <210> SEQ ID NO: 13

273 <211> LENGTH: 262

274 <212> TYPE: DNA

275 <213> ORGANISM: Conus aurisiacus

277 <400> SEQUENCE: 13

278	ggatccatga	tgtctaaact	gggagtccttg	ttgaccatct	gtctacttct	gtttccctt	60
280	actgcttttc	cgatggatgg	agatcaacct	gcagaccaac	ctgcagatcg	tatgcaggac	120
282	gacatttcat	ctgagcagta	tcccttggtt	gataagagac	aaaagtgttg	cactgggaag	180
284	aaggggtcat	gctccggcaa	agcatgcaaa	aatctcaaat	gttgctctgg	acgataacgt	240
286	gttgatgacc	aactttctcg	ag				262

289 <210> SEQ ID NO: 14

290 <211> LENGTH: 78

RAW SEQUENCE LISTING

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291 <212> TYPE: PRT
 292 <213> ORGANISM: Conus aurisiacus
 294 <400> SEQUENCE: 14
 296 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 297 1 5 10 15
 299 Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
 300 20 25 30
 302 Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
 303 35 40 45
 305 Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
 306 50 55 60
 308 Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 309 65 70 75
 311 <210> SEQ ID NO: 15
 312 <211> LENGTH: 23
 313 <212> TYPE: PRT
 314 <213> ORGANISM: Conus aurisiacus
 316 <220> FEATURE:
 317 <221> NAME/KEY: PEPTIDE
 318 <222> LOCATION: (1)..(23)
 319 <223> OTHER INFORMATION: Xaa at residue 1 is Gln or pyro-Glu
 322 <400> SEQUENCE: 15
 324 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 325 1 5 10 15
 327 Lys Asn Leu Lys Cys Cys Ser
 328 20
 330 <210> SEQ ID NO: 16
 331 <211> LENGTH: 232
 332 <212> TYPE: DNA
 333 <213> ORGANISM: Conus aurisiacus
 335 <400> SEQUENCE: 16
 336 ggatccatga tgtctaaact gggagtcttg ctgaccatct gtctgcttct gtttccaactt 60
 338 actgctgttc cgctggatgg agatcaacct ctagaccgac acgcggagcg tatgcatgat 120
 340 ggcatttcac cttaaagcca tccctggtt gatcccgta aacggtgttg caaggtgcaa 180
 342 tgcgagtctt gcaccccttg ttgctaactg gttgatgacc aactttctcg ag 232
 345 <210> SEQ ID NO: 17
 346 <211> LENGTH: 68
 347 <212> TYPE: PRT
 348 <213> ORGANISM: Conus aurisiacus
 350 <400> SEQUENCE: 17
 352 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 353 1 5 10 15
 355 Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Leu Asp
 356 20 25 30
 358 Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro
 359 35 40 45
 361 Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys
 362 50 55 60
 364 Thr Pro Cys Cys

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/910,009

DATE: 08/01/2001

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Input Set : A:\2314-242.ST25.txt

Output Set: N:\CRF3\08012001\I910009.raw

L:21 M:270 C: Current Application Number differs, Replaced Current Application No
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:1390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:1447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:1506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:1567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78
L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
L:1685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:1741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93
L:1915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:96
L:1990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99
L:2068 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:2071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:2090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:2150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106
L:2209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109
L:2274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:112

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L:2332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115
L:2389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121